SEQUENCE LISTING

<110> Andrade-Gordon, Patricia
Darrow, Andrew
Qi, Jenson

<120> DNA encoding the human serine protease T

<130> ORT-1032

<140>
<141>

<160> 9

<170> PatentIn Ver. 2.0

<210> 1
<211> 1110
<212> DNA
<213> Homo sapiens

<400> 1

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ccaggatgct gaaccgaatg gtgggcgggc aggacacgca ggagggcgag tggccctggc 180

aagtcagcat ccagcgcaac ggaagccact tctgcggggg cagcctcatc gcggagcagt 240

gggtcctgac ggctgcgcac tgcttccgca acacctctga gacgtccctg taccaggtcc 300

tgctgggggc aaggcagcta gtgcagccgg gaccacacgc tatgtatgcc cgggtgaggc 360

aggtggagag caacccccctg taccagggca cggcctccag cgctgacgtg gccctggtgg 420

agctggaggc accagtgccc ttcaccaatt acatcctccc cgtgtgcctg cctgacccct 480

cggtgatctt tgagacgggc atgaactgct gggtcactgg ctggggcagc cccagtgagg 540

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ccaagtgcaa cctgctctac agcaaagaca ccgagttttgg ctaccaaccc aaaaccatca 660

agaatgacat gctgtgcgcc ggcttcgagg agggcaagaa ggatgcctgc aagggcgact 720

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ggggtgaggg ctgtgcccgc cagaaccgcc caggtgtcta catccgtgtc accgcccacc 840

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agaagtgaga cccccggggc caggagcccc ttgagcagag ctctgcaccc agcctgcccg 960

cccacaccat cctgctggtc ctcccagcgc tgctgttgca cctgtgagcc ccaccagact
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1080
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1110

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 2

gccaggcctg aggacatgag 20

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 3

tgcgctggat gctgacttgc 20

<210> 4

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nested probe

<400> 4

ccaggatgct gaaccgaatg gtgggcgggc aggacacgca 40

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 5

aggatctaga ggaggcgag tggccctggc 30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 6

ggggtctaga cttctggccg cccaacctcg 30

<210> 7

<211> 290

<212> PRT

<213> Homo sapiens

<400> 7

Met Arg Arg Pro Ala Ala Val Pro Leu Leu Leu Leu Leu Cys Phe Gly
1 5 10 15

Ser Gln Arg Ala Lys Ala Ala Thr Ala Cys Gly Arg Pro Arg Met Leu
20 25 30

Asn Arg Met Val Gly Gly Gln Asp Thr Gln Glu Gly Glu Trp Pro Trp

35 40 45

Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser Leu

50 55 60

Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn Thr

65 70 75 80

Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu Val

85 90 95

Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu Ser

100 105 110

Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu Val

115 120 125

Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val Cys
130 135 140

Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp Val
145 150 155 160

Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro Arg
165 170 175

Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys Asn
180 185 190

Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr Ile
195 200 205

Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp Ala
210 215 220

Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln Ser
225 230 235 240

Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg Gln
245 250 255

Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp Ile
260 265 270

His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly Gly
275 280 285

Gln Lys
290

<210> 8

<211> 1130

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion gene of Protease T in a zymogen activation vector

<400> 8

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gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac 120

gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctat 180

gctctagagg agggcgagtg gccctggcaa gtcagcatcc agcgcaacgg aagccacttc 240

tgcgggggca gcctcatcgc ggagcagtgg gtcctgacgg ctgcgcactg cttccgcaac 300

acctctgaga cgtccctgta ccaggtcctg ctggggcaaa ggcagctagt gcagccggga 360

ccacacgcta tgtatgcccg ggtgaggcag gtggagagca acccccctgta ccagggcacg 420

gcctccagcg ctgacgtggc cctggtggag ctggaggcac cagtgccctt caccaattac 480

atcctccccg tgtgcctgcc tgaccctcg gtgatctttg agacgggcat gaactgctgg 540

gtcactggct ggggcagccc cagtgaggaa gacctcctgc ccgaaccgcg gatcctgcag 600

aaactcgctg tgccatcat cgacacaccc aagtgcaacc tgctctacag caaagacacc 660

gagtttggct accaacccaa aaccatcaag aatgacatgc tgtgcgccgg cttcgaggag 720

ggcaagaagg atgcctgcaa gggcgactcg ggcggccccc tggtgtgcct cgtgggtcag 780

tcgtggctgc aggcgggggt gatcagctgg ggtgagggct gtgcccgcca gaaccgccca 840

ggtgtctaca tccgtgtcac cgcccaccac aactggatcc atcggatcat ccccaaactg 900

cagttccagc cagcgaggtt gggcggccag aagtctagac atcaccatca ccatcactag 960

cggccgcttc cctttagtga gggttaatgc ttcgagcaga catgataaga tacattgatg 1020

agtttggaca aaccacaact agaatgcagt gaaaaaaatg ctttatttgt gaaatttgtg 1080

atgctattgc tttatttgta accattataa gctgcaataa acaagttgac 1130

<210> 9

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein of Protease T in a zymogen activation construct

<400> 9

Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu
1 5 10 15

Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys

20 25 30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp

35 40 45

Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Glu Gly Glu Trp Pro

50 55 60

Trp Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser

65 70 75 80

Leu Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn

85 90 95

Thr Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu

100 105 110

Val Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu

115 120 125

Ser Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu
130 135 140

Val Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val
145 150 155 160

Cys Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp
165 170 175

Val Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro
180 185 190

Arg Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys
195 200 205

Asn Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr
210 215 220

Ile Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp

225 230 235 240

Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln

245 250 255

Ser Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg

260 265 270

Gln Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp

275 280 285

Ile His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly

290 295 300

Gly Gln Lys Ser Arg His His His His His His

305 310 315